

GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: March 17, 2003, 08:47:27 ; Search time 35 Seconds  
(without alignments)  
4580.133 Million cell updates/sec

Title: US-10-010-227-3

Perfect score: 4055

Sequence: 1 MCGAESTPQTLVDKVLQAHV.....KAVPVPPTNRGEEKPELW 778

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

## Database :

SPTREMBL\_21:\*  
1: sp archaea:\*  
2: sp bacteria:\*  
3: sp fungi:\*  
4: sp human:\*  
5: sp invertebrate:\*  
6: sp mammal:\*  
7: sp mhc:\*  
8: sp organelle:\*  
9: sp phage:\*  
10: sp plant:\*  
11: sp rodent:\*  
12: sp virus:\*  
13: sp vertebrate:\*  
14: sp unclassified:\*  
15: sp virus:\*  
16: sp bacteriap:\*  
17: sp archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	length	DB	ID	Description
1	2432.5	60.0	711	3	Q9P3Y5	Q9P3Y5	Yarrowia li
2	1636	40.3	469	16	Q9ZL76	Q9ZL76	Rhizobium m
3	1611	39.7	469	16	Q8YJC9	Q8YJC9	Brucella me
4	1586	39.1	475	16	Q8UBV9	Q8UBV9	Agrobacteri
5	1567.5	38.7	469	16	Q9SEB1	Q9SEB1	Rhizobium l
6	1563	38.5	448	2	Q9EV53	Q9EV53	Rhizobium m
7	1562	38.5	479	16	Q9ABN0	Q9ABN0	Caulobacter
8	1548.5	38.2	469	16	Q9JZ15	Q9JZ15	Neisseria m
9	1545.5	38.1	469	16	Q9JUB2	Q9JUB2	Neisseria m
10	1507.5	37.0	474	16	Q9HZA3	Q9HZA3	Pseudomonas
11	1498.5	37.0	474	16	Q9PAX0	Q9PAX0	Xylella fas
12	1493	36.8	469	16	Q8XXX3	Q8XXX3	Ralstonia s
13	1469.5	36.2	466	16	Q8XA00	Q8XA00	Escherichia
14	1452	35.8	476	16	Q8ZIH0	Q8ZIH0	Yersinia pe
15	1425.5	35.2	467	16	Q9KPB1	Q9KPB1	Vibrio chol
16	1396	34.4	472	16	Q9K8P0	Q9K8P0	Bacillus ha

17	1385.5	34.2	476	16	Q86534	Q86534	Streptomyce
18	1354.5	33.4	466	2	Q85072	Q85072	Buchnera ap
19	1354	33.4	469	2	Q85065	Q85065	Buchnera ap
20	1315.5	32.4	448	2	Q9EVF9	Q9EVF9	Buchnera ap
21	1311.5	32.3	470	16	Q9P1M1	Q9P1M1	Campylobact
22	1290.5	31.8	466	2	Q31293	Q31293	Buchnera ap
23	1283.5	31.7	462	16	Q92A26	Q92A26	Listeria in
24	1282	31.6	456	16	Q92A26	Q92A26	Listeria in
25	1280.5	31.6	442	2	Q9EVA1	Q9EVA1	Staphylococ
26	1279.5	31.6	442	16	Q8Y5R7	Q8Y5R7	Listeria ap
27	1275.5	31.5	443	2	Q9EVI0	Q9EVI0	Listeria mo
28	1271.5	31.4	444	2	Q9EVI8	Q9EVI8	Buchnera ap
29	1259.5	30.9	443	2	Q9EVI5	Q9EVI5	Buchnera ap
30	1253.5	30.9	443	2	Q9EVI6	Q9EVI6	Buchnera ap
31	1252.5	30.9	442	2	Q9EVI3	Q9EVI3	Buchnera ap
32	1244.5	30.7	436	2	Q9AJ49	Q9AJ49	Buchnera ap
33	1240.5	30.6	436	2	Q9AJ48	Q9AJ48	Buchnera ap
34	1238.5	30.5	436	2	Q99073	Q99073	Buchnera ap
35	1236.5	30.5	436	2	Q9AJ47	Q9AJ47	Buchnera ap
36	1236.5	30.5	443	2	Q9EVA4	Q9EVA4	Buchnera ap
37	1230.5	30.3	436	2	Q9AJ52	Q9AJ52	Buchnera ap
38	1227.5	30.3	442	2	Q9EVA7	Q9EVA7	Buchnera ap
39	1225.5	30.2	444	2	Q9EVB0	Q9EVB0	Buchnera ap
40	1222.5	30.1	433	2	Q99009	Q99009	Buchnera ap
41	1217.5	29.9	473	16	Q8ZKJ0	Q8ZKJ0	Salmonella
42	1211.5	29.9	442	2	Q9EVA2	Q9EVA2	Buchnera ap
43	1209.5	29.8	472	2	Q9ZND5	Q9ZND5	Thermus the
44	1194.5	29.5	456	2	Q9A1M3	Q9A1M3	Streptococc
45	1172.5	28.9	467	16	Q8YX02	Q8YX02	Anabaena sp
46	1170.5	28.9	418	2	Q9AJ50	Q9AJ50	Buchnera ap
47	1065.5	26.3	369	2	Q9AQC6	Q9AQC6	Buchnera ap
48	699.5	17.3	418	17	Q8TVF2	Q8TVF2	Methanopyru
49	660	16.3	424	17	Q8TLE1	Q8TLE1	Methanosarc
50	656.5	16.2	424	17	Q8UZA1	Q8UZA1	Pyrococcus
51	641	15.8	431	16	Q9PTI6	Q9PTI6	Deinococcus
52	640.5	15.8	659	16	Q67656	Q67656	Aquifex aeo
53	637.5	15.7	423	17	Q9U207	Q9U207	Pyrococcus
54	627.5	15.5	174	2	Q8VMA6	Q8VMA6	Rhizobium e
55	612.5	15.1	641	16	Q8RCF8	Q8RCF8	Thermomanae
56	599	14.8	642	16	Q97KE8	Q97KE8	Clostridium
57	597.5	14.7	211	16	Q8YCW7	Q8YCW7	Brucella me
58	595.5	14.7	417	16	Q9WZ24	Q9WZ24	Rhizobium l
59	586.5	14.5	201	16	Q98BS1	Q98BS1	Rhizobium
60	576.5	14.2	422	16	Q97EB0	Q97EB0	Clostridium
61	570.5	14.1	509	10	Q94AR8	Q94AR8	Methanosarc
62	562	13.9	420	17	Q8TQZ3	Q8TQZ3	Halobacteri
63	562	13.9	661	17	Q9HMF1	Q9HMF1	Agrobacteri
64	560.5	13.8	216	16	Q8UBR0	Q8UBR0	Arabidopsis
65	558.5	13.8	509	10	Q9TOL4	Q9TOL4	Rhizobium m
66	555.5	13.7	201	16	Q92LA1	Q92LA1	Schizosacch
67	552	13.6	721	3	Q9UT74	Q9UT74	Neisseria m
68	544	13.4	213	16	Q9JUB1	Q9JUB1	Pseudomonas
69	542	13.4	212	16	Q9HZA4	Q9HZA4	Pseudomonas
70	542	13.4	213	16	Q9JZ16	Q9JZ16	Neisseria m
71	541.5	13.4	418	16	Q9WTC7	Q9WTC7	Thermotoga
72	536.5	13.2	777	3	Q96VU1	Q96VU1	Aspergillus
73	535	13.2	216	16	Q8XXX4	Q8XXX4	Ralstonia s
74	533	13.1	201	2	Q8RP98	Q8RP98	Methylobact
75	523.5	12.9	418	2	Q9ZNE0	Q9ZNE0	Thermus the
76	519	12.8	215	16	Q9PAX1	Q9PAX1	Xylella fas
77	513	12.7	202	16	Q9ABN1	Q9ABN1	Caulobacter
78	512	12.6	434	16	Q9RTY9	Q9RTY9	Deinococcus
79	511.5	12.6	418	16	Q8RDK2	Q8RDK2	Thermomanae
80	506	12.5	201	16	Q8Z9I3	Q8Z9I3	Salmonella
81	500.5	12.3	201	16	Q9CJN8	Q9CJN8	Pasteurella
82	498	12.3	200	16	Q9XP80	Q9XP80	Vibrio chol
83	492	12.1	201	16	Q8XA01	Q8XA01	Escherichia
84	482.5	11.9	768	4	Q9UGZ0	Q9UGZ0	Homo sapien
85	474.5	11.7	780	4	Q8TAQ6	Q8TAQ6	Homo sapien
86	474	11.7	200	16	Q8ZIH1	Q8ZIH1	Yersinia pe
87	473.5	11.7	780	11	Q99K10	Q99K10	Mus musculu
88	472.5	11.7	780	11	Q9ER34	Q9ER34	Rattus norv
89	472.5	11.7	787	5	Q9NFX1	Q9NFX1	Drosophila

90 470.5 11.6 778 3 074699  
 91 467 11.5 194 16 Q9R8F1  
 92 463 11.4 905 3 Q9P7D4  
 93 457 11.3 809 3 Q9HEA5  
 94 455 11.2 788 5 Q9NG03  
 95 447 11.0 415 17 Q8ZM41  
 96 442.5 10.9 747 2 Q8R8P7  
 97 442 10.9 683 5 Q9VIE8  
 98 441 10.9 402 17 Q8TW29  
 99 440 10.9 415 17 Q974R0  
 100 438 10.8 196 2 Q9AIM2

## ALIGNMENTS

RESULT 1  
 Q9P3Y5  
 ID Q9P3Y5 PRELIMINARY; PRT; 711 AA.  
 AC Q9P3Y5;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE 3-isopropylmalate dehydratase (EC 4.2.1.33) (Fragment).  
 GN LEU1.  
 OS Yarrowia lipolytica (Candida lipolytica).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Dipodascaceae; Yarrowia.  
 OX NCBI\_TaxID=4952;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R22;  
 RX MEDLINE=21382182; PubMed=11489863;  
 RA Mautersberger S., Wang H., Gaillardin C., Barth G., Nicaud J.M.,  
 RT "Insertional mutagenesis in the n-alkane-assimilating yeast Yarrowia  
 RT lipolytica: generation of tagged mutations in genes involved in  
 RT hydrophobic substrate utilization."  
 RL J. Bacteriol. 183:5102-5109(2001).  
 DR EMBL; AJ278693; CAB99455.1; -  
 DR InterPro; IPR000573; Aconitase\_C.  
 DR InterPro; IPR001030; Aconitase\_N.  
 DR InterPro; IPR001899; Gram\_pos\_anchor.  
 DR InterPro; IPR004430; Leuc.  
 DR InterPro; IPR004431; Leuc.  
 DR Pfam; PF00330; aconitase; 1.  
 DR PRINTS; PR00694; Aconitase\_C; 1.  
 DR PRODOM; PD000511; Aconitase\_N; 1.  
 DR TIGRFAMs; TIGR00170; leuc; 1.  
 DR TIGRFAMs; TIGR00171; leuc; 1.  
 DR PROSITE; PS00450; ACONITASE\_1; 1.  
 DR PROSITE; PS01244; ACONITASE\_2; 1.  
 DR PROSITE; PS00343; GRAM\_POS\_ANCHORING; UNKNOWN\_1.  
 KW Lyase.  
 FT NON\_TER  
 SQ SEQUENCE 711 AA; 77476 MW; 996407A7F7B1AF2E CRC64;

Query Match  
 Best Local Similarity 60.0%; Score 2432.5; DB 3; Length 711;  
 Matches 480; Conservative 76; Mismatches 130; Indels 45; Gaps 9;  
 QY 9 QLYDKVLQAHVDEKLDGTVLYIDRLHVEVTSPOAFGLRNAGKVRPDCITLATD 68  
 DB 3 QLYDKVFAHDVHHED - NGYLLFIDRLHVEVTSPOAFGLRNAGKVRKDCITLATD 61  
 QY 69 HNVPTTSRKALDIASFIKEDDSRTCVTEENNVKFGVTFYGLSDKRGVHVHVGEEQ 128  
 DB 62 HNIPTTRKDFKSGIFKEEDSRLCTTLEQNVKFGVTFYGMDDKRGVHVHVGEEQ 121  
 QY 129 FTLPGTVVCGDSHTSHGAFALAFIGTSEVHVLATQCLITKRSKNRIQVDGELAP 188  
 DB 122 FTLPGTVVCGDSHTSHGAFALAFIGTSEVHVLATQCLITKRSKNRIQVDGELAP 181

QY 189 GVSSKDVVLHAIGTITAGCTGAVIEFCGSVTRSLSNARMSTCNMSIEGAGRMVAPD 248  
 DB 182 GITSKDLILHIIIGVIGTAGGTGTVIEFCGEARDLSMEARMSMCNMAIEGAGRMVAPD 241  
 QY 249 EITFEVLGRPLAPKYDSEWHEKATQYKWNLOSDPCAKYDIDYFIDAKDITVPLTWGTS 308  
 DB 242 EITFYIRGRPLAP - EGAWEKAVTYKWLHSDSDAEFDIDVNIKGEDIIPTVTWTS 299  
 QY 309 EDVPIITGVVDPETFAFEAKKADGRMLQYMGKAGTMEIDIPVQKVFIGSCTNSRIED 368  
 DB 300 QDALPITGVDPKESDPIKEAGIERALEYMGLEANTPLNEIAVDKVFIGSCTNSRIED 359  
 QY 369 LRAAAAVKGRKANPVKSAMVVPVPSGLVKTQABEEGLDKIPFEAGFEWREAGSCMLGM 428  
 DB 360 LRAAAAVIRGKKKADSVVRAMVVPVPSGLVKRAEAEGLDKVFEAAGFEWREAGSCMLGM 419  
 QY 429 NPDILAPOERCASSTNRNPEGRGAGGRPHLMSPVMAAAGIVGKLADVR - - - - - KL 480  
 DB 420 NPDILNPRECASTNRNPEGRGAGGRPHLMSPVMAAAGIVGKLADVR - - - - - 479  
 QY 481 T - - - - - DYKASPHIAAYQKSTVTKPH - VDERINQDAHEKDIADIPEDNNGPH 527  
 DB 480 VIGEDEEMAEAKYDEEKQPAVKMKMTATVTQADPVDEQTDVAEE - - - - - 524  
 QY 528 TNSASVGTSGAGLPKFTILKIGIAAPLEKANVDTDAIIPKQFLTKIKRTGLGNALFVEMRF 587  
 DB 525 -NITSS - - - - - ATGIPKFLVSGIAAPLPKANVDTDAIIPKQFLTKIKRTGLSSGLFFEWRF 580  
 QY 588 NE-DG - TEKSDFLVANKPEYRKASILVCTGANTGCGSSREHAPWALNDFGIRSVIAPSPAD 645  
 DB 581 KEVDQKQKTDPMNVAPWDPWDKASILVSGNFGCGSSREHAPWALNDFGIRSVIAPSPAD 640  
 QY 646 IFFNNSFKNGMLPIPIKQAOIEAIAAARAGKEIVDLPNQLIKNAKGITICTFEVEEF 705  
 DB 641 IFFNNSFKNGMLPIPIKQAOIEAIAAARAGKEIVDLPNQLIKNAKGITICTFEVEEF 700  
 QY 706 RKHCLVNGLDD 716  
 DB 701 RKHCRVNGLDD 711  
 RESULT 2  
 Q92L76 PRELIMINARY; PRT; 469 AA.  
 ID Q92L76;  
 AC Q92L76;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Probable 3-isopropylmalate dehydratase large subunit protein  
 DE (EC 4.2.1.33).  
 GN LEUC OR R03206 OR SMC03823.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Goidre T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Rameger U.,  
 RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 RT Sinorhizobium meliloti strain 1021".  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 DR EMBL; AL591793; CAC47785.1; -  
 DR InterPro; IPR001030; Aconitase\_N.  
 DR InterPro; IPR004430; Leuc.  
 DR Pfam; PF00330; aconitase; 1.  
 DR ProDom; PD000511; Aconitase\_N; 1.  
 DR TIGRFAMs; TIGR00170; leuc; 1.

ID	Q8UB99	PRELIMINARY;	PRT;	475 AA.
AC	Q8UB99;			
DT	01-JUN-2002 (TREMBLrel, 21, Created)			
DT	01-JUN-2002 (TREMBLrel, 21, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel, 21, Last annotation update)			
DE	3-Isopropylmalate dehydratase, large subunit.			
GN	LEBC OR ATU2709 OR AGR_C_4910.			
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970).			
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Rhizobiaceae; Rhizobium.			
OX	NCBI_TaxID=176299;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21608550; PubMed=11743193;			
RA	Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,			
RA	Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,			
RA	Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D. Sr.,			
RA	Chapman P., Clendenning U., Deatherage G., Gillet W., Grant C.,			
RA	Rayavavin T., Levy R., Li M.-i., McClelland E., Palmeri A.,			
RA	Katsumata C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,			
RA	Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,			
RA	Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,			
RA	Chumley F., Tingey S.V., Toml J.-F., Gordon M.P., Olson M.V.,			
RA	Nester E.W.;			
RT	"The genome of the natural genetic engineer Agrobacterium tumefaciens			
RT	C58".;			
RL	Science 294:2317-2323 (2001).			
RN	[2]			



DR EMBL; AJ296268; CAC14578.1; -;  
 DR InterPro; IPR001030; Aconitase\_N.  
 DR InterPro; IPR004430; Leuc.  
 DR Pfam; PF00330; aconitase; 1.  
 DR PRINTS; PR00415; ACONITASE\_N; 1.  
 DR ProDom; PD000511; Aconitase\_N; 1.  
 DR TIGRFAMs; TIGR00170; leuc; 1.  
 DR PROSITE; PS00450; ACONITASE\_1; 1.  
 DR PROSITE; PS01244; ACONITASE\_2; UNKNOWN\_1.  
 DR Isoemase.  
 KW NON\_TER  
 FT SEQUENCE 448 AA; 48466 MW; 029B65EA51A054BD CRC64;  
 SQ  
 Query Match 38.5%; Score 1563; DB 2; Length 448;  
 Best Local Similarity 66.1%; Pred. No. 2,6e-97;  
 Matches 300; Conservative 53; Mismatches 93; Indels 8; Gaps 3;  
 QY 26 DGVLLYIDRLVHEVTSPOAFEGLRNAGKRVRRPDDCTLATTDHNVPTTSRKALKDIASF 85  
 DB 1 DGTCLLYIDCHLVHEVTSPOAFEGLRNAGKRVRAPEKTLAVVDHNVPTSPDRHLG----- 55  
 QY 86 IKEDDSRTQCVTLEENVKEFGVTFGLSDKRGIVHVI GPEGGFTLPGTTVCGDSHTST 145  
 DB 56 IKNESRLOVEALRNAAADLGEVYSENDKRGIVHVI GPEGGFTLPKMTIVCGDSHTST 115  
 QY 146 HGAFGALAFGIGTSEVEHVLATQCLITRKSKRMRIQVDELAPGVSSKDVLAHIGIT 205  
 DB 116 HGAGGALAHGIGTSEVEHVLATQTLQKKAKNMLVRVDGQ.PPGVTADIIALIGEIGT 175  
 QY 206 AGGTGAVIEFGSVIRISLSMEARMSICMSIEGARGAMVAPDETTFEYLRKRLAPKYD 265  
 DB 176 AGGTGHVIEFGAEIRISLSMEGRMTVCMMTIEGARGALVAPDETTFEYLRKRLAPKYD 235  
 QY 266 SPEHKAATQWKKNLOSDBGAKYDIDVFIDAKDVIPTLTMTGSPEDVVPITGVPPETFA 325  
 DB 236 A--NDRAVEYKTLHMDGAHYDVRVLDANLPPIVSGSSPELVVSVQGVPPDDIQ 293  
 QY 326 TEAKKADGRMLQYWGGLKAGTPEMDIPVDKVFISGCTNSRIEDLRPAAAVYGRKKAPNV 385  
 DB 294 DETKRTSKMRALDVGGLRPGTKITDIAIDRVIGSCTNGRIEDLRPAVVEVGRKSPFV 353  
 QY 386 KSAMVPPSGGLVTKQAEBSGLDKITEFGKFEWREAGCSKCLGMNDIILAPORCASTNR 445  
 DB 354 -SAMIVPSSGLVKEQAEABGLDKIFKEAGFDWREPGCSKCLAMNDRLKPGERCASTNR 412  
 QY 446 NEEGRGAGGRTHLMSPVMAAAGIVGKLADVRK 479  
 DB 413 NEEGRGGRKTRHLSPMVMAAAGVGHFVDIRE 446  
 RESULT 7  
 Q9ABNO PRELIMINARY; PRT; 479 AA.  
 ID Q9ABNO  
 AC Q9ABNO; 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DN 3-isopropylmalate dehydratase, large subunit.  
 GN CC0196.  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;  
 OC Caulobacter.  
 OC NCBI\_TaxID=15892;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RC MEDLINE=21173698; PubMed=11259647;  
 RX Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Oha N., Maddock J.R.,  
 RA Pococka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
 RA Kolonay J.F., Smit J., Crahen M.B., Khouri H., Shetty J., Berry K.,  
 RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 RT "Complete genome sequence of Caulobacter crescentus";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 DR EMBL; AE005694; AAK22183.1; -;  
 DR TIGR; CC0196; -;  
 DR InterPro; IPR001030; Aconitase\_N.  
 DR InterPro; IPR004430; Leuc.  
 DR Pfam; PF00330; aconitase; 1.  
 DR PRINTS; PR00415; ACONITASE.  
 DR ProDom; PD000511; Aconitase\_N; 1.  
 DR TIGRFAMs; TIGR00170; leuc; 1.  
 DR PROSITE; PS00450; ACONITASE\_1; 1.  
 DR PROSITE; PS01244; ACONITASE\_2; UNKNOWN\_1.  
 DR Complete proteome.  
 KW SEQUENCE 479 AA; 50693 MW; BE19EB931A251BFA CRC64;  
 SQ  
 Query Match 38.5%; Score 1562; DB 16; Length 479;  
 Best Local Similarity 64.4%; Pred. No. 3,3e-97;  
 Matches 307; Conservative 53; Mismatches 105; Indels 12; Gaps 5;  
 QY 9 QTLVDKVLQAHVVDKLDGTVLLYIDRLVHEVTSPOAFEGLRNAGKRVRRPDDCTLATTD 68  
 DB 4 KTLVDKIDAHVVS-AGGEALIVYIDLHLIHEVTPQAFAGLRAGKRVRRPDDTLAVAD 62  
 QY 69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTFGLSDKRGIVHVI GPEGG 128  
 DB 63 HNPTEGALGVDA--VADEARLQLTLARNVADNIEFPWGDINNGIVHVGPEGG 119  
 QY 129 FTLPGTVCGDSHTSTGAFGALAFGIGTSEVEHVLATQCLITRKSKRMRIQVDELAP 188  
 DB 120 RTQPMNTIVCGDSHTSTGAFGALAHGIGTSEVEHVLATQTLQKKAKNMLVRVDGQ.PP 179  
 QY 189 GVSXKDVVLAHIGIIGTAGTGAIVIEFGSVIRISLSMEARMSICMSIEGARGAMVAPD 248  
 DB 180 GVTGKDVLAIVIEGIGTAGTGYVIEFGAEIAGLSMEGRMTLCMTIEGKAKALVAPD 239  
 QY 249 ETTFEYLRKRLAPKYDSEPHKAATQWKKNLOSDBGAKYDIDVFIDAKDVIPTLTMTGSP 308  
 DB 240 DKTFAVIGKPAAPK--GAAMDALSHWKTFTDPAVFDRTVIDGSALVPMVTWGSTP 297  
 QY 309 EDVVPITGVPPETPATEAKKADGRMLQYWGGLKAGTPEMDIPVDKVFISGCTNSRIED 368  
 DB 298 EDVIVTGNVPDPESFALPDKRAAHRALDVGGLKAGGPISARIDRVIGSCTNSRIED 357  
 QY 369 LRAAAVYK----GRKAPNVKSAVVPGSLVTKQAEBSGLDKITEFGKFEWREAGCS 423  
 DB 358 MRAAAVQAEALHGRVLAAPHVK-AMVVPSSGLVKEQAEBSGLDAIFRAAGPDMREPGCS 416  
 QY 424 MCLGNPDLIAQERCASTSNRNEFGROGAGRTLMSPVMAAAGIVGKLADVRKL 480  
 DB 417 MCLAMPDKLAPQERCASTSNRNEFGROGAGRTLVSPMAAALAHGLVDVRTL 473  
 RESULT 8  
 Q9JZT5 PRELIMINARY; PRT; 469 AA.  
 ID Q9JZT5  
 AC Q9JZT5; 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DN 3-isopropylmalate dehydratase, large subunit.  
 GN NMB1036.  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OC NCBI\_TaxID=491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MC58 / SEROGROUP B;  
 RC MEDLINE=20175755; PubMed=10710307;  
 RX Tettelein H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
 RA Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,  
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

RX	MEDLINE=20222556; PubMed=10761919;
RA	Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA	Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA	Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.
RA	Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA	Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA	Whitehead S., Spratt B.G., Barrrell B.G.
RT	"Complete DNA sequence of a serogroup A strain of Neisseria
RT	meningitidis Z2491."
RL	Nature 404:502-506(2000).
DR	EML; ALI62756; CAB84686.1; -.
DR	InterPro; IPR001030; Aconitase_N.
DR	IncerPro; IFR004430; LeucC.
DR	Fram; PF00330; acnaitase; 1.
DR	PRINTS; PR00415; ACONITASE.
DR	Pf-dom; PD00511; Aconitase_N; 1.
DR	TIGRFAMS; TIGR00170; leuC_I.
DR	PROSITE; PS00450; ACONITASE_1; 1.
DR	PROSITE; PS01244; ACONITASE_2; 1.
KW	Lysase; Complete proteome.
SQ	SEQUENCE 469 AA; 50783 MW; 89AE349827DA35DB CRC64;
	Query Match 38.1%; Score 1545.5; DB 16; Length 469;
	Best Local Similarity 63.4%; Pred.No. 4.2e-96;
	Matches 301; Conservative 62; Mismatches 103; Indels 9; Gaps
QY	7 TPQTLYDKVLQAHVVEKLDGTVLLYIDRHLLVHEVTSPQAFGLRWAGRKVRPDCDTLAT 66
Db	2 TAQTLTKLWNHSHVREEDGTVLLYIDRHLLVHEVTSPQAFGLKWAGRDKWRIDSWSWT 61
QY	67 TDHNVPITSRKALKDITASFTIKEDDSRTCVCVTLEENVKEFG-VTYFGLSKRGIVHHVGIP 125
Db	62 ADHWTF-----GDWDKGIDPIFKLVQVDLTDNKFEGCALAYFFPMQGGQIVHMVGP 115
QY	126 EQGFTLPGMTWCSDSHTSTHGAFGALAFIGTSEVHEVLATQCILTRKSKNMRIODGE 185
Db	116 EQGATLPGMTWCSDSHTSTHGAFGALAHGI GTSEVHTMATCIITA KSKSLIAVDGK 175
QY	186 LAGVSCKDVVLAHGI GTAGTGAVIFPCGSVIRLSWEARMSICNMSIEGGAPAGNV 245
Db	176 LKAGVTAKDVALVII GOIGTAGTGVAIBFGGEAIRLSMEGRMTLCNNMAIEAARGSMV 235
QY	246 APDEITPEYLKGRFLAPKYDSPWHKATOYKKNLQDPGAKYDIDVIDAKDIVPLPTWG 305
Db	236 AVDTTTIDYVKDFEAGEA--WDKA VEYWRITVSYDEGAVDFKEYRNAEDIEPOVTWG 293
QY	306 TSDEDVPIGVVDDPETATEKAKADGRMI QYMGLKAGTWEDIPVDKVFI GSCTNR 365
Db	294 TSPENVLDISSKYPNPAAETBDPVKRSGMERALEYMGLEAGTFLNEIPVDIVFGSCTNR 353
QY	366 IEIDLAAAAVVKRKKAPNKVASMPVPSGLVKVTOAEEBGLDKI FEEAGFEWREGCSMC 425
Db	354 VEDLRGAALAKDRKKAANQRVLI IVPGSSLVKEQAKEGLDKI FEAGFEWREGCSMC 413
QY	426 LGNPPDILA PQERCASTSNRNFEGRGAGRRTHLMSPVNAAAAGIVGLADVRKL 480
Db	414 LANNADELTPGORCASTSNRNFEGRGCGRRTHLVSPAMAAAAAATGRTDIRMM 468



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QY 369 LRAAAVVKRKPAPNVKSMVPGSLVKTQAEEGGLDKIFEBAGFEWREAGCSMCLGM 428
D 361 LRAAAEVVKRKPASTVTKQAMVPGSLVKAQAEVEGLDKIFEBAGFEWREPGCSMCLAM 420
QY 429 NPDLAPQERCASTSNRNFEGRGAGGRTHLMSVMAAAAGIVGKLADVRKL 480
D 421 NPKLGSGEHCASSTSNRNFEGRGIGGRTHLVSPAMAAAAAAGVDFVDVREM 472

RESULT 12
Q8XXX3 PRELIMINARY; PRT; 469 AA.
AC Q8XXX3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable 3-isopropylmalate dehydratase (Large subunit) protein
DE (EC 4.2.1.33).
GN LEUC OR RSC1990 OR RS03558.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brotier P., Camus J.C., Cattolico L.,
RA Chandler C., Choise N., Clauzel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646067; CAD15692.1; -.
DR InterPro; IPR001030; Aconitase_N.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR PRODOM; PD000511; aconitase_N; 1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR LYase; Complete proteome.
SQ SEQUENCE 469 AA; 50796 MW; B451E96E44788AAE CRC64;

Query Match 36.8%; Score 1493; DB 16; Length 469;
Best Local Similarity 63.5%; Pred. No. 1.5e-92;
Matches 301; Conservative 53; Mismatches 110; Indels 10; Gaps 3;

QY 9 QTLVDKVLQAHVDEKLDGTVLLYIDRLVHEVTSPOAFGLRNAGRKVRPDCCTLATTD 68
D 3 KTLVDKLDHVVHTEDEGTVLLYIDRLVHEVTSPOAFGLKLANRPWRISANLAVSD 62
QY 69 HNVPTTSRKALKDIASFKEKDDSRQCVTLLENVKEFGVTYFGLSKRQGIHVHIGPEQG 128
D 63 HNVPTTDR-----SHGIADPVSKLOVDLTLDNCDSFGITQFKMTDKRQGIHVHIGPEQG 116
QY 129 FTLPGTTVVCGDSHTSTHGAFALAGFISGTHVEHLVATQCLITKRSKNMRIQVDGELAP 188
D 117 ATLPGMTTVVCGDSHTSTHGAFALAGHIGTSEVHLVATQTLAKKSNMLVKVEGTLP 176
QY 189 GVSSKDWLHAIGITGAGTGAVIRPCGVSIRSLMEARMSICNMSIEGARAGMVAPD 248
D 177 GCTAKDIVLAIGKITAGTGAVMEFGGSAIRALSMEGRMTVCNMAIEAGARAGMVGD 236
QY 249 EITFEYKGRPLAPKDYDSPWHKATQWKNLQSDPGAKYDIDVFIDAKDIPVTLTWGTSP 308
D 237 DITLEYIKGRPPAPQ--GVMEQAVAYWRSLSHSDGARFHDVHVELRAEIRPQVSWGTSP 294
QY 309 EDVVPITGVVDPDETATEKAKDGRMLQYMGKAKTGMEDIPVDKVFVFGSCNTSRIED 368
D 309 EDVVPITGVVDPDETATEKAKDGRMLQYMGKAKTGMEDIPVDKVFVFGSCNTSRIED 368
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D 295 EMVTSIEDRVDPDKEDPVKNAMERALEYVALQPNVAIGDIRIDKIVFGSCNTSRIED 354
QY 369 LRAAAAVVK--GRKAPNVKSMVPGSLVKTQAEEGGLDKIFEBAGFEWREAGCSMCL 426
D 355 MRAAAVWVQKLGKRTASNVKLAAMVPGSLVKEQAEREGLDKIFKAAGFEWREPGCSMCL 414
QY 427 GNPDPILAPQERCASTSNRNFEGRGAGGRTHLMSVMAAAAGIVGKLADVRKL 480
D 415 ANNADRLPEFGERCASTSNRNFEGRGAGGRTHLVSPAMAAAAAALGHHFVDVRKL 468

RESULT 13
Q8XA00 PRELIMINARY; PRT; 466 AA.
AC Q8XA00;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 3-isopropylmalate isomerase (dehydratase) subunit.
GN LEUC OR Z0081 OR ECS0076.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posaf J.G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005184; AAG54376.1; -.
DR EMBL; AP002550; BAB33499.1; -.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; Leuc.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR PRODOM; PD000511; aconitase_N; 1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR Isomerase; Complete proteome.
SQ SEQUENCE 466 AA; 49898 MW; 4722550F4C7772EA CRC64;

Query Match 36.2%; Score 1469.5; DB 16; Length 466;
Best Local Similarity 61.9%; Pred. No. 5.6e-91;
Matches 292; Conservative 59; Mismatches 112; Indels 9; Gaps 4;

QY 9 QTLVDKVLQAHVDEKLDGTVLLYIDRLVHEVTSPOAFGLRNAGRKVRPDCCTLATTD 68
D 3 KTLVEKFDHVLHVFAEENETPLLYIDRLVHEVTSPOAFGLRAHGRPVQPGKTFATMD 62
QY 69 HNVPTTSRKALKDIASFKEKDDSRQCVTLLENVKEFGVTYFGLSKRQGIHVHIGPEQG 128
D 63 HNVSTQT---KDNAC--GEMARIQMQLKCNKEFGVELYDLNHPYQGIHVHIGPEQG 116
QY 129 FTLPGTTVVCGDSHTSTHGAFALAGFISGTHVEHLVATQCLITKRSKNMRIQVDGELAP 188
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Db 117 VTLGKMTIVCGDSHTATGAFGALAFGIGTSEVEHVLTATQTLKQGRATMKIEVQGAAP 176
Qy 189 GVSSKDVVLAHIGIIGTAGTGAIVFPGSVIRSLSEARMSICNMSIEGARAGMVPD 248
Db 177 GITAKDIYLAIIIGKTSAGSGTGHVFEFCGEAIRDLSMEGRMLCNMALEMGAQGLVAPD 236
Qy 249 EITFEYLKGRPLAPKYDSEPMHKAQYWKNIQSDPAKYDIDVFIDAKDIYVTLTWGTSF 308
Db 237 EITFEYVYGRHLAPK--GKDFDDAAVAYWKTLOTDEGATFDVTVLQABEISPOYWTGNP 294
Qy 309 EDVYPIITGVVDEPFEATKAKDGRMLQYWGGLAGTPEMEIIPVDKXIFIGCTSRIED 368
Db 295 GQVIVSVDNIDPDPASFADPVERASAEKALAYWGLKPGILTEVAIDKXIFIGSCTSRIED 354
Qy 369 LRAAAVYVGRKKAPNVYSAMVPGSGLVKTOAESEGDLKIPFEEAGFEWREAGSCMCLGM 428
Db 355 LRAAAEIKKGRKVAFGVQ-ALVVPSSGPVKAQAEAGLDKXIFIEGFEKRLPGCSMCLAM 413
Qy 429 NPDLAPQERCASTSNRNFEGROGAGRTHLMSPVMAAAGIVGLADYVKL 480
Db 414 NNDRLNPERCASTSNRNFEGROGGRGRTHLVSPMAAAAATGHPADIRNI 465

RESULT 14
Q8ZIH0 PRELIMINARY; PRT; 476 AA.
AC 08ZIH0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33).
GN LEUC OR YPO0531.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OC NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RA MEDLINE=21470413; PubMed=11586360;
RA Packhili J., Wren B.W., Thomson N.R., Tlball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagsels K., Kariyasev A.V.,
RA Leather S., Mouton S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,
RA "Genome sequence of Yersinia pestis, the causative agent of plague.";
RA EMBL: AJ141413; CAC89388.1;
RL Nature 413:523-527(2001).
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; Leuc.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR Kyrase; Complete proteome.
SQ SEQUENCE 476 AA; 50589 MW; 052D8ED2165E5E74 CRC64;

Query Match 35.8%; Score 1452; DB 16; Length 476;
Best Local Similarity 59.2%; Pred. No. 8.9e-90;
Matches 289; Conservative 66; Mismatches 121; Indels 12; Gaps 5;

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Qy 121 HVIEGEGFTLPETTVCAGDSHTSHGAFGALAFGIGTSEVEHVLTATQCLTKSKMNI 180
Db 115 HVIEGEGMTLPGMTIVCGDSHTATHGAFGSLAFGIGTSEVEHVLTATQTLKQGRATKRI 174
Qy 181 QVDEGLAVGSSKDVVLAHIGIIGTAGTGAIVFPGSVIRSLSEARMSICNMSIEGARAGMVPD 240
Db 175 EVNGTVGAGITAKDIYLAIIIGKTSAGSGTGHVFEFCGEAIRDLSMEGRMLCNMALEMGA 234
Qy 241 RAGVAPDEITFEYLKGRPLAPKYDSEPMHKAQYWKNIQSDPAKYDIDVFIDAKDIYV 300
Db 235 KAGLVAPDDITFAVYKQGFAP--TGEQMEGVAYMRLTKSDADQFPTIYVLDAADLAP 292
Qy 301 TLTWGTSEDVVPITGVVDPDEPTEAKKADGRMLQYWGGLAGTPEMEIIPVDKXIFIGS 360
Db 293 QVTWGTNGQVIAVNOIIPAESEFSDPVERASAEKALAYMDLPKIKLTEVAIDKXIFIGS 352
Qy 361 CTNSRIEDLRAAAAVKGRKAPNVYSAMVPGSGLVKTOAESEGDLKIPFEEAGFEWRE 420
Db 353 CTNSRIEDLRAAAALAQGRKVAQVQ-ALVVPSSGPVKAQAEAGLDKXIFIAAGFEWRLP 411
Qy 421 GCSMCLGMNPDLAPQERCASTSNRNFEGROGAGRTHLMSPVMAAAGIVGLADYVKL 480
Db 412 GCSMCLAMNDRLEBERCASTSNRNFEGROGGRGRTHLVSPMAAAAATGHPADIRNI 471
Qy 481 TDYKASPH 488
Db 472 S---ATTH 476

RESULT 15
Q9KP81 PRELIMINARY; PRT; 467 AA.
AC 09KP81;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 3-isopropylmalate dehydratase, large subunit.
GN VC2492.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OC NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N1691 / SEROTYPE O1;
RA MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Niernan W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004318; AAP95634.1;
DR TIGR; VC2492;
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; Leuc.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR Kyrase; Complete proteome.
SQ SEQUENCE 467 AA; 50185 MW; 4F7607148FA85ADD CRC64;

Query Match 35.2%; Score 1425.5; DB 16; Length 467;
Best Local Similarity 58.9%; Pred. No. 5.3e-88;
Matches 279; Conservative 67; Mismatches 119; Indels 9; Gaps 4;

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QY 6 STPOTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPOAFEGRLNAGRKVRPDCCTLA 65
DB 2 SKAKTLYEKIYDAHVVAAPGETPILYIDRHLVHEVTSPOAFDGLRKGPRVQVSKTFA 61
QY 66 TTDHNPVTSRKALKDIASTPIKEDDSRTQCVTLLENVKEFGVTYFGLSDKROGTVHVIGP 125
DB 62 TMDHNVSTTT-----KQINA--SGEMARIQMTLSKNCSEFGVTLYDINHXYQGIHVHWGP 115
QY 126 EQGFTLPGTTVCGDSTHTSHGAFALAFGIGTSEVEHVLATQCLITKRSKNMIRIQVDGE 185
DB 116 ELGITLPGMTIVCGDSTHTSHGAFALAFGIGTSEVEHVLATQCLITKRSKNMIRIQVDGE 175
QY 186 LAPGVSQDVVLAHGIIGTAGGTGAVIEFCGVSIRLSWEARMSICNMSIEGGARAGMV 245
DB 176 VAPGITAKDILVLAIGKTTAAGGTGYVVEFCGEAIRLSMEGRMTVCNMAIELGAKAGLI 235
QY 246 APDEITFEYLKGRPLAPKYDSPWHKATQYWKNLQSPGAKYDIDVFIDAKDIIPTLTWGS 305
DB 236 APDATTFNKIGRKFAPQ--GSDWDAADVYQTLKTDDEAQFDVAVVLEASEIKPQVTWG 293
QY 306 TSPEDVVPITGVVDPDETFAATEAKADGRRLMQLYMGKAGTTPMEDIPVDKVFISCTNSR 365
DB 294 TNPQVIADVDEPSPSQFADPVERSAAEKALAYMGLGKMLSDYKVDKVFVGSCTNSR 353
QY 366 IEDLRAAAVVKGRKAPNVKSMVVPGLVKTQAEELGDKTIFEBAGFEWRAGCSMC 425
DB 354 IEDMRAAAVAKGKVASHVQ--ALIVPSPQVKAQAEELGDKTIFEBAGFEWRPLPGCSMC 412
QY 426 LGMNPDILAPQERCASTSNRNFEGRCAGGRTHLMSVMAAAAGIVGKLADVR 479
DB 413 LAMNDRLGFGERCASSTSNRNFEGRCAGGRTHLMSVMAAAAGIVGKLADVR 466
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RESULT 16
Q3K8FO
ID Q9K8FO PRELIMINARY; PRT; 472 AA.
AC Q9K8FO
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit [EC 4.2.1.33].
GN LEUC OR BHJ056.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331 (2000).
DR EMBL; AP001517; BAB06775.1; -
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; Leuc.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PD000415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR Lyase; Complete proteome.
SQ SEQUENCE 472 AA; 50886 MW; 79D8A588C293F981 CRC64;
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Query Match 34.4%; Score 1396; DB 16; Length 472;
Best Local Similarity 59.2%; Pred. No. 5.3e-86;
Matches 279; Conservative 58; Mismatches 124; Indels 10; Gaps 3;
QY 8 POTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPOAFEGRLNAGRKVRPDCCTLAT 67
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DB 3 PKTIEKLDWDAHTVIGEKGPSLLYIDHMHVEVTSPOAFEGRLNAGRKVRPDLTATM 62
QY 68 DHNVPTTSRKALKDIASTPIKEDDSRTQCVTLLENVKEFGVTYFGLSDKROGTVHVIGPEQ 127
DB 63 DHNVPTVDPRNIQD-----QIARKQIETLEANCKEFGIEIAGLSDSPNGGIVHVIGPEL 115
QY 128 GFTLPGTTVCGDSTHTSHGAFALAFGIGTSEVEHVLATQCLITKRSKNMIRIQVDGE 187
DB 116 GLTQPGKTIIVCGDSTHTSHGAFALAFGIGTSEVEHVLATQCLITKRSKNMIRIQVDGE 175
QY 188 PGVSKQDVVLAHGIIGTAGGTGAVIEFCGVSIRLSWEARMSICNMSIEGGARAGMV 247
DB 176 PVSAAKDIILAVIAKYGVDFGTGHVIEFTGEAIRLSMEERMTICNMSIEAGAKAGLISP 235
QY 248 DEITFEYLKGRPLAPKYDSPWHKATQYWKNLQSPGAKYDIDVFIDAKDIIPTLTWGS 307
DB 236 DSVTFEYLGRPNAPKGEA--FDVAIQWEALATAGAVYDRLVLMNASEIEPMTWTG 293
QY 308 PEDVVPITGVVDPDETFAATEAKADGRRLMQLYMGKAGTTPMEDIPVDKVFISCTNSRIE 367
DB 294 PAQGTGVSVVPSPPDAKDENERRAIKQSLAYMGLPGTPTETAIQHVIFIGSCTNSRLS 353
QY 368 DLRAAAVVKGRKAPNVKSMVVPGLVKTQAEELGDKTIFEBAGFEWRAGCSMC 427
DB 354 DLRTAAELIKGRKQVADGVR--ALVWFGSQVQKRAAEKEGLDEIFKEAGFEWRDSCSMCLG 412
QY 428 MNPDILAPQERCASTSNRNFEGRCAGGRTHLMSVMAAAAGIVGKLADVR 478
DB 413 MNPDTVPEGERCASTSNRNFEGRCAGGRTHLMSVMAAAAGIVGKLADVR 463
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RESULT 17
O86534
ID O86534 PRELIMINARY; PRT; 476 AA.
AC O86534
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 3-isopropylmalate dehydratase large subunit.
GN LEUC OR SC0553 OR SC1C2.34.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Murphy L., Harris D.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96 (1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
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Query Match	Best Local Similarity	Score	DB 2	Length	466
Matches 268; Conservative 74; Mismatches 121; Indels 9; Gaps	56.8%;	Pred. No. 3.3e-83;			
9 QTLRYKVLQAHVYNDKLDGTVLLYIDRLVHVNVSPOAFEGLRNAGKVRPDPCTLATTD	33.4%;	1354.5;	DB 2;	Length 466;	
3 KTLRYKIVDSHVHSEKGLSTLYVDLHMLHVTSPQAFESLRIDRYRQKPKFATMD					
69 HNVPTSRKALKDIASTFKEDDSRTQCVTLLENVKEFGVTFGLSDKRGQIVHVGPEEG					
63 HNVSTSE-----KDINA--SGSWAKIQMOQLRNCKEFHISTLYDLNHPNOGIHVHISPEEG					
129 FTLPGTTVCGDSHSTHGAFGALAFGISTSEVENYALAQCLITRSKRMRIQVDELAP					
117 MTLPGVAVICGSHSTHGAFGALAFGISTSEVENYALATQTLKQDFKMKLEVIQKIGN					
189 GVSSKDVVLAIGITAGTAGVAVIEFCGVSIRLSMEARMSIUNNISIEGARAGVAVDP					
177 FITADVILYITIGKIGSSAGTGYIIIEFCGNVKKKSMERMVTCNNVAIELGAKSGLIAD					
249 EITFEYLKGRPLAPKYDSEPMHKATQYWKNSLQSDPAKXIDIVFDIAKQIVPLTLGTSP					
237 ETLTYLAKKKTSP--HGRNMOKALIEYWKTLKTDHNAIFDKVFTTIDISILPLQVTLGTFN					
309 EDVVPITGVVPDEPFAFEAKKADGRRLQYMGKLGKTFMEDIPVDKVFISGCTNSRIED					
295 DQYTGINEKIPDTSIQNVKKDLAKSACKMDLKRGTIYITDITDKVFIQCTNSRIED					
369 LRAAAIVVKKRKKAPNVKSMVYVGGGLVKTQAESEGLDKIFEEDAGEEWFACGSCMLG					
355 LRASAKILKHNKIKSKNVK-AIVVPGGLVYRQAESEGLDKIFEEDAGEEWFACGSCMLG					
429 NPDILAPQERCASTSNRNPEGRGAGRRITLMPWMAAAAGIYGLADYKTL					
414 NNDRLENERCASTSNRNPEGRGRRGRITLVPPIVALALALIGKFSNPYKL					
RESULT 19					
085065	PRELIMINARY;	PRT;	469 AA.		
AC	085065;				
DT	01-NOV-1998 (TREMBLrel). 08, Created)				
DT	01-NOV-1998 (TREMBLrel). 08, last sequence update)				
DT	01-JUN-2002 (TREMBLrel). 21, last annotation update)				
DE	Isopropylmalate isomerase subunit.				
OS	LEUC.				
OS	Buchnera aphidicola.				
OC	Plasmid pIen-Sg.				
OC	Bacteria; Proteobacteria; gamma subdivision; Buchnera.				
OX	NCBI_Taxid=9;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9091706; PubMed=9873079;				
RA	Baumann U., Baumann P., Moran N.A., Sandstrom J., Thao M.L.;				
RT	"Genetic characterization of plasmids containing genes encoding				
RT	enzymes of leucine biosynthesis in endosymbionts (Buchnera) of				
RT	aphids."				
RL	J. Mol. Evol. 48:77-85 (1999).				
DR	EMBL; AF041836; AAD12595.1; --.				

[illegible]

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DR InterPro: IPR004430; leuc.
DR Pfam: PF00330; aconitase; 1.
DR PRINTS: PR00415; ACONITASE_N; 1.
DR ProDom: PD000511; Aconitase_N; 1.
DR TIGRFAMs: TIGR00170; leuc; 1.
DR PROSITE: PS00450; ACONITASE_1; 1.
DR PROSITE: PS01244; ACONITASE_2; 1.
DR Complete proteome.
SQ SEQUENCE 470 AA; 51710 MW; 48FEA523C94337D9 CRC64;

Query Match
Best Local Similarity 32.3%; Score 1311.5; DB 16; Length 470;
Matches 264; Conservative 65; Mismatches 131; Indels 13; Gaps 4;

OY 9 QTLVKVLAHVVDKLDGTVLLYIDRLVHEVTSPOAFEGRLNAGRKRRPDCATATD 68
DB 5 KLYEKFPAHVVEGKNLPILYIDRLHIEVTSPOAFSGLMARRRRAADLTATTD 64
OY 69 HNVPTTSR--KALKDIASITKEDDSRTQCVLEENYKEFGVTFGLSDPKRQGIHVHIGPE 126
DB 65 HDVSTKSMDLNCSDA-----KEQITLTMQNTKEGVLGLGDKXQGIHVHIGPE 116
OY 127 QGFTLPGTVCGSDSHSTHGAFGALAFGIGTSEVEHVALATQCLITKSKNMRIOVDGEL 186
DB 117 LGFTLPGVTLVCGSDSHSTHATGAFGALAFGIGTSEVEHVALATQCLITKSKNMRIOVDGEL 176
OY 187 AFGVSSKDVLAHGIITGAGTGAIVIEFGSVIRSLSEARMSICNMSIEGARAGMVA 246
DB 177 QKGVYTKDILLYIAOYGAFTAGTGYAIEFGSELIRNLSMARMTLCMALEFAKGMIA 236
OY 247 PEITFEYKGRRLAKKYSPSEMHKATQYKNSLPDGAKYDIVFIDAKDIVPTLTWTGT 306
DB 237 PEITFEYKGRRLAKKYSPSEMHKATQYKNSLPDGAKYDIVFIDAKDIVPTLTWTGT 294
OY 307 SPEDVVPITGVDPDEFATKAKKADGRMLQYMGKAGTPEMEDIPIVUKVFIGSTNSRI 366
DB 295 NPSQVIGIDEKIKISDFKQKQSKSLDALYVYNLEQDQVIEGVKIDIVFIGSTNGRL 354
OY 367 EDIRAAAVVKKRKAQVNVKAMVYPSGIVKTOAESEGLDKIPEEGFEMREACSCICM 426
DB 355 EDIKIADILKGRKIKHNVK-ALIVPSMQVRKEAENLIGDKIFIEGCEWRVAGCMCL 413
OY 427 GNMPLDLPQERCASTSNRNFEGROGAGRTHLMSPVMAAAGIVGLADVRK 479
DB 414 GNMDDKANSQGVASTSNRNFVGRQKGSITHLMSPVMAAAGIVGLADVRK 466

RESULT 22
O31293 PRELIMINARY; PRT; 466 AA.
AC O31293;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 3-isopropylmalate dehydratase subunit.
GN LEUC.
OS Buchnera aphidicola.
OC Bacteriia; Proteobacteria; gamma subdivision; Buchnera.
OC NCBI_TaxId=9;
OX [1]
RN SEQUENCE FROM N.A.
MEDLINE=97386415; PubMed=9244264.
RA Van Ham R.C.H.U., Moya A., Latorre A.;
RT "putative origin of plasmids carrying the genes involved in leucine
RT biosynthesis in Buchnera aphidicola (endosymbiont of aphids).";
RL J. Bacteriol. 179:4768-4777(1997).
DR EMBL: Y11966; CAJ2703.1; -.
DR InterPro: IPR001030; Aconitase_N.
DR InterPro: IPR004430; leuc.
DR Pfam: PF00330; aconitase; 1.
DR PRINTS: PR00415; ACONITASE.
DR ProDom: PD000511; Aconitase_N; 1.

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DR TIGRFAMs: TIGR00170; leuc; 1.
DR PROSITE: PS00450; ACONITASE_1; 1.
DR PROSITE: PS01244; ACONITASE_2; 1.
DR Pfam: PF00330; aconitase; 1.
DR Complete proteome.
SQ SEQUENCE 466 AA; 51930 MW; A63877597C846ADB CRC64;

Query Match
Best Local Similarity 31.8%; Score 1290.5; DB 2; Length 466;
Matches 261; Conservative 65; Mismatches 137; Indels 9; Gaps 4;

OY 9 QTLVKVLAHVVDKLDGTVLLYIDRLVHEVTSPOAFEGRLNAGRKRRPDCATATD 68
DB 3 QTLVKVLAHVVDKLDGTVLLYIDRLVHEVTSPOAFEGRLNAGRKRRPDCATATD 62
OY 69 HNVPTTSR--KALKDIASITKEDDSRTQCVLEENYKEFGVTFGLSDPKRQGIHVHIGPE 128
DB 63 HNVSTTKN-----ISASGA--AQIQMOQLINCCDFNKLVDLHININGIYHVMGPEOG 116
OY 129 FTLPGTVVCGSDSHSTHGAFGALAFGIGTSEVEHVALATQCLITKSKNMRIOVDGELAP 188
DB 117 LTLPGVTLVCGSDSHSTHGAFGALAFGIGTSEVEHVALATQCLITKSKNMRIOVDGELAP 176
OY 189 GYSSKDVLAHGIITGAGTGAIVIEFGSVIRSLSEARMSICNMSIEGARAGMVA 248
DB 177 YITAKVILLYIIKKVGTAGTGYVIEFGSEITENLTBEGMTICNNVIEGAKSGIATD 236
OY 249 EITFEYKGRRLAKKYSPSEMHKATQYKNSLPDGAKYDIVFIDAKDIVPTLTWTGTSP 308
DB 237 ATTYKILKMLPVAPKE--KMKNALEYKMLKTDNDKIDKIVFVSGIETWTMP 294
OY 309 EDVVPITGVDPDEFATKAKKADGRMLQYMGKAGTPEMEDIPIVUKVFIGSTNSRIED 368
DB 295 SQTINITESPDKKINNIIIDKQATEKALKYMLKPNOKIMLVVKKVFIGSTNSRIED 354
OY 369 LRRAAAVVKRKAQVNVKAMVYPSGIVKTOAESEGLDKIPEEGFEMREACSCICM 428
DB 355 LRASKIIKKRKAQVNVK-ALIVPSKLYKIQAEKGLDKIFINAGFEMRLPSCSNCLAM 413
OY 429 NPDILAPQERCASTSNRNFEGROGAGRTHLMSPVMAAAGIVGLADVRK 480
DB 414 NDKIKRNGECASTSNRNFEDRQGRGRTHLVSPITAAAALIGYFVDIKNI 465

RESULT 23
O92A26 PRELIMINARY; PRT; 462 AA.
AC O92A26;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Leuc protein.
GN LEUC OR LIN2096.
OS Listeria innocua.
OC Bacteriia; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxId=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / SEROVAR 5A;
RX PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Ruenick C., Amend A.,
RA Bagueri F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Cherouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurgeat O.,
RA Entian K.-D., Feibi H., Garcia-del Portillo F., Garrido P.,
RA Gautier U., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft U., Kuhn M., Kunst F., Kutzapart G.,
RA Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).

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DR EMBL; AL596171; CAC97326.1; -.
DR Listlist; LIN02096; -.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; Leuc.
DR Pfam; PF00330; aconitase; 1.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; UNKNOWN_1.
DR PROSITE; PS01244; ACONITASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 462 AA; 51041 MW; 0F09F51E77F0B4B2 CRC64;

Query Match 31.7%; Score 1283.5; DB 16; Length 462;
Best Local Similarity 53.3%; Pred. No. 2e-78;
Matches 251; Conservative 72; Mismatches 129; Indels 19; Gaps

QY 9 QTLYDKVLQAHVDEKLDGTVLLYIDRLHVEHTSPQAFGLRNAGKVRPDCPTLATTD 68
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
3 KTLFDKLNHRHVIYKGEQEPQLLYIDLHLIHEVTSPQAFGLRNAGKVRPDCPTLATMD 62
QY 69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLLENVKEFGVTYFGLSDKRQGIHVHVGPEQG 128
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
63 HNVPTEDIFNIQDLV-----AKQIEALQTNCEEFGVTLADMGSDRQGIHVHVGPETG 115
QY 129 FTLPCTTVVCGDSHTSHGAFALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP 188
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
116 LTQPGKIVVCGDSHTATHGAFGAIFGIGTSEVEHVFATQTLWQTKPKNLKIDINGTLPT 175
QY 189 GVSSKDVLLHAIGIAGTAGTGAIVFCGVSIRLSMEARMSICNMIEGGARAGWVAPD 248
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
176 GVYAKDIIHLIATYGVAFGTGVAVEYGTIRMSMEERTICNMIEGGARAGWVAPD 235
QY 249 EITFEYKGRPLAPKYDPSPEHMKATQYWKLOSDPKAKYDIDVFIKADIVPTLTWTGTS 308
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
236 QTFTEYVGRREYAPS----DMKAIKRWETLKTDPDAEYDLHIEMDASILEPVTWTGTP 291
QY 309 EDVVPITGVVPDETFATEAKKADGRMLQYMGKAGTPEMDIPVKVFTGSCNTRIED 368
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
292 EMGVPSKAPF-----ETKDMYERAYEYMGKPGQTAEIEELGVVFTGSCNTRIED 344
QY 369 LRAAAAVVGRKKAPNVKSAWVPGSLVKTQAEIEGLDKIFEEAGFEWREAGCSCLGM 428
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
345 LEEAARIVKGNKYKNIR-ALVVGSRQVNAEAEIGLDFKIDAGFEWREPCSCMLGM 403
QY 429 NPDLAPQERCASTSNRNFEGRQAGRTHLMSFVMAAAGIVGKLADVRK 479
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
404 NPQVDPDGVHCASTSNRNFEGRQAGRTHLVSPAMAAAAAINGHFIIDIRK 454

RESULT 24
Q99SJ3 PRELIMINARY; PRT; 456 AA.
AC Q99SJ3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE 3-isopropylmalate dehydratase large subunit.
GN LEUC OR SAV2059 OR SAI864.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OC Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_taxid=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
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RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240 (2001).
DR EMBL; AF003364; BAB58221.1; -.
DR EMBL; AF003364; BAB43146.1; -.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; Leuc.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 456 AA; 50326 MW; 4C2D584937186ECC CRC64;

Query Match 31.6%; Score 1282; DB 16; Length 456;
Best Local Similarity 54.4%; Pred. No. 2.5e-78;
Matches 257; Conservative 64; Mismatches 131; Indels 20; Gaps

QY 9 QTLYDKVLQAHVDEKLDGTVLLYIDRLHVEHTSPQAFGLRNAGKVRPDCPTLATTD 68
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
3 QTLFDKLNHRHVIYKGEFQLLYIDLHLIHEVTSPQAFGLRNAGKVRPDCPTLATLD 62
QY 69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLLENVKEFGVTYFGLSDKRQGIHVHVGPEQG 128
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
63 HNVPTI-----DIFN-IKDETANKOITLQKNAIDFGVHIFDMGSDQGIHVHVGPETG 115
QY 129 FTLPCTTVVCGDSHTSHGAFALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP 188
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
116 LTQPGKTIIVCGDSHTATHGAFGAIFGIGTSEVEHVFATQTLWQTKPKNLKIDINGTLPT 175
QY 189 GVSSKDVLLHAIGIAGTAGTGAIVFCGVSIRLSMEARMSICNMIEGGARAGWVAPD 248
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
176 GVYAKDIIHLIATYGVDFGTGVALEFTGETTKNLSMDGRMTICNMIEGGARAGWVAPD 235
QY 249 EITFEYKGRPLAPKYDPSPEHMKATQYWKLOSDPKAKYDIDVFIKADIVPTLTWTGTS 308
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
236 DITFEYVKGPRPADNF-----AKSVDKWRELYSDDDAIFDRVIELDVSTLEPQVTTGTP 290
QY 309 EDVVPITGVVPDETFATEAKKADGRMLQYMGKAGTPEMDIPVDKVFIGSCNTRIED 368
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
291 EMGVNFSEPPF-----EINDINDQRAYDMGLEPGQAEIDILGYVFLGSCNTRIED 343
QY 369 LRAAAAVVGRKKAPNVKSAWVPGSLVKTQAEIEGLDKIFEEAGFEWREAGCSCLGM 428
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
344 LLEASHIVKGNKVHPNI-TAIVVPGSRVTYKAEKLGDTIFKNAGFEWREPCSCMLGM 402
QY 429 NPDLAPQERCASTSNRNFEGRQAGRTHLMSFVMAAAGIVGKLADVRKL 480
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
403 NPQVDPDGVHCASTSNRNFEGRQAGRTHLVSPAMAAAAAINGHGFVDVRKV 454

RESULT 25
Q99VH1 PRELIMINARY; PRT; 442 AA.
AC Q99VH1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Isopropylmalate dehydratase subunit (Fragment).
GN LEUC.
OS Buchnera aphidicola.
OC Bacterium; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_taxid=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20576185; PubMed=11133977;
RA Wernegreen J.J., Moran N.A.;
RT "Vertical transmission of biosynthetic plasmids in aphid endosymbionts
```

RT (Buchnera)";  
J. Bacteriol. 183:785-790(2001).  
DR EMBL; AF197453; AAG31394.1; "-  
DR InterPro; IPR001030; Aconitase\_N.  
DR InterPro; IPR004430; Leuc.  
DR Pfam; PF00330; aconitase; 1.  
DR PRINTS; PR00415; ACONITASE.  
DR ProDom; PD000511; Aconitase\_N; 1.  
DR TIGRFAMs; TIGR00170; leuc; 1.  
DR PROSITE; PS00450; ACONITASE\_1; 1.  
DR PROSITE; PS01244; ACONITASE\_2; 1.  
DR Plasmid.  
KW  
SQ SEQUENCE 442 AA; 442  
FT MON TER 49589 MW; 7ACBE7267AC18982 CRC64;

Query March 31.6%; Score 1280.5; DB 2; Length 442;  
Best Local Similarity 56.0%; Pred. No. 3e-78;  
Matches 252; Conservative 74; Mismatches 113; Indels 11; Gaps 5;

QY 9 QTLVYKVLQAHVYDEKLDGTLLVYIDRLVHEVTSPOAFEGIRNAGKVRKRRPDCLTATTD 68  
DB 3 KTLVYKIVSHIVYNDQEKTSILYIDLHLHEVTSPOAFESLRNKRKRVROPNKTFAIMD 62  
QY 69 HNVPTSRKALDI-ASFIKEDDSRTQCVLTLENVKEFGVTYFGLSDKRQGIHVHIGPEQ 127  
DB 63 HNVSTQT---KDINASGLM--AQKQMEQLKNCNEFNISLYDINHPRQGIHVHIADES 115  
QY 128 GFTLPQTIVVCGDSHTSTHGAFGALAFGIGTSEVHVLATQCLITRSKMRIOVDGELA 187  
DB 116 GMTLPMTIVCGDSHTSTHGAFGALAFGIGTSEVHVLATQCLITRSKMRIOVDGELA 175  
QY 188 PGVSSKDVVLHAIIGITGAGTGAVIEFGGSVIRSLMEARMSICNMSIEGARGAMVAP 247  
DB 176 KFTVAKDIIIFITGKLGTSAGSYVEFCGKTIKRMSEERMTICNMALEMGAKSGLIEP 235  
QY 248 DETTFEYKGRPLAPKYDSPEWHKATQYWNLOSPGAKYIDVFIADKDIVFTLTWGS 307  
DB 236 DETTAYLKNKITSFR--GLFWQSINWMDLTKSDKDAYFDKFTIDISNLAFOITWGT 293  
QY 308 PEDVVPITGVPPDETFATEAKKADGRMLQYGLKAGTMEIDIPVDKVFISCTNSRIE 367  
DB 294 PDQVISIDEKIPNVEEENCLVKNAKASACEYWGKPDYLTLDIDKVFISCTNARIIE 353  
QY 368 DLRAAAAVVGRKKAIPVYKSAWVPGSLVKTQAEFEGLDKIFEEAGFEWREAGCSWCLG 427  
DB 354 DLRSASITLKNKVSNNK-AIVVPGSLVKTQAEKEGLDKIFIDSGFEWRLPGCSWCLG 412  
QY 428 MNPDLAPQERCASTSNRNFEGROGAGRT 457  
DB 413 MNRDLISFGERCASXSNRNFEGRGGRGT 442

Search completed: March 17, 2003, 08:50:17  
Job time : 50 secs

